

SEQUENCE LISTING

<110> KREUTZER, CAROLINE  
MOCKEL, BETTINA  
PFEFFERLE, WALTER  
EGGELING, LOTHAR  
SAHM, HERMANN  
PATEK, MIROSLAV

<120> L-LYSINE PRODUCING CORYNEBACTERIA AND  
PROCESS FOR THE PREPARATION OF LYSINE

<130> 21123/278416/MAS

<140> 09/810,521

<141> 2001-03-19

<150> DE 199 31314.8

<151> 1999-05-07

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> -35\_signal

<222> (774)..(779)

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<223> DNA upstream from dapB

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tcgggtatcg	atacctggaa	cgacaacctg	atcaggatat	ccagtgcctt	gaatatgac	180
gttgagggaag	gaatcaccag	ccatctcaac	tggaaagcct	gacgcctgct	gaattggatc	240
agtggcccaa	tcgacccacc	aaccagggtg	gccattaccg	gcgatatcaa	aaacaactcg	300
tgtgaacgtt	tcgtgctcgg	caacgcggat	gccagcgatc	gacatatcgg	agtcaccaac	360
ttgagcctgc	tgcttctgat	ccatcgacgg	ggaacccaac	ggcggcaaa	cagtggggga	420
aggggggag	ttggtgcact	ctgaaccgag	tggctcttga	agtggtaggc	gacggggcag	480
ctatctgaag	gcgtgcgagt	tgtggtgacc	gggttagcgg	tttcagtttc	tgtcacaact	540
ggagcaggac	tagcagaggt	tgtaggcggt	gagccgcttc	catcacaagc	acttaaaagt	600
aaagaggcgg	aaaccacaag	cgccaaggaa	ctactcgcca	acggggcggt	aaaggccaact	660
taagtctcat	atttcaaaac	tagttccacc	tgtgtgatta	atccctagaa	cggaacaaac	720
tgatgaacaa	tcgttaacaa	cacagaccaa	aacggtcagt	taggatgga	tatcagcacc	780
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<212> DNA

<213> Corynebacterium glutamicum

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Val	Gly	Gln	Thr	Ile	Val	Ala	Ala	Val	Asn	Glu	Ser	Asp	Asp	Leu	Glu	
	15					20					25					
ctt	ggt	gca	gag	atc	ggc	gtc	gac	gat	gat	ttg	agc	ctt	ctg	gta	gac	985
Leu	Val	Ala	Glu	Ile	Gly	Val	Asp	Asp	Asp	Leu	Ser	Leu	Leu	Val	Asp	
30					35					40					45	
aac	ggc	gct	gaa	gtt	gtc	gtt	gac	ttc	acc	act	cct	aac	gct	gtg	atg	1033
Asn	Gly	Ala	Glu	Val	Val	Val	Asp	Phe	Thr	Thr	Pro	Asn	Ala	Val	Met	
				50					55					60		

ggc aac ctg gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga 1081  
 Gly Asn Leu Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly  
 65 70 75

acc acg ggc ttc gat gat gct cgt ttg gag cag gtt cgc gac tgg ctt 1129  
 Thr Thr Gly Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu  
 80 85 90

gaa gga aaa gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc 1177  
 Glu Gly Lys Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile  
 95 100 105

tct gcg gtg ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc 1225  
 Ser Ala Val Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe  
 110 115 120 125

gaa tca gct gaa gtt att gag ctg cac cac aac aag ctg gat gca 1273  
 Glu Ser Ala Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala  
 130 135 140

cct tca ggc acc gcg atc cac act gct cag ggc att gct gcg gca cgc 1321  
 Pro Ser Gly Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg  
 145 150 155

aaa gaa gca ggc atg gac gca cag cca gat gcg acc gag cag gca ctt 1369  
 Lys Glu Ala Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu  
 160 165 170

gag ggt tcc cgt ggc gca agc gta gat gga atc ccg gtt cat gca gtc 1417  
 Glu Gly Ser Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val  
 175 180 185

cgc atg tcc ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag 1465  
 Arg Met Ser Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln  
 190 195 200 205

ggt cag acc ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt 1513  
 Gly Gln Thr Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe  
 210 215 220

gca cca ggt gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc 1561  
 Ala Pro Gly Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly  
 225 230 235

cta gtc gta gga ctt gag cat tac cta ggc ctg taaaggctca ttccagcagc 1614  
 Leu Val Val Gly Leu Glu His Tyr Leu Gly Leu  
 240 245

ggggtgaatt ttttaaaagg agcgttttaa ggctgtggcc gaacaagtta aattgagcgt 1674

ggagttgata gcgtgcagtt cttttactcc acccgctgat gttgagtgt caactgatgt 1734

tgagggcgcg gaagcactcg tcgagtttgc gggctgtgccc tgctacgaaa cttttgataa 1794

gccgaaccct cgaactgctt c 1815

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 Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala  
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 Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala  
 35 40 45  
 Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu  
 50 55 60  
 Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly  
 65 70 75 80  
 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys  
 85 90 95  
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val  
 100 105 110  
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala  
 115 120 125  
 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly  
 130 135 140  
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala  
 145 150 155 160  
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser  
 165 170 175  
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser  
 180 185 190  
 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr  
 195 200 205  
 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly  
 210 215 220  
 Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val  
 225 230 235 240  
 Gly Leu Glu His Tyr Leu Gly Leu  
 245

<210> 4  
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<400> 7  
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<212> DNA  
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<220>  
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Primer

<400> 8  
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<210> 9  
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<212> DNA  
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<220>  
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<210> 10  
<211> 19  
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<220>  
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<400> 12  
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<400> 13  
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<400> 17  
ccaaatgagg gaagaaggta taattgaact ctatgagca 39

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